

PF gene

XX claim 2: Page 18: 41pp: English.

XX The present sequence is the 5' region of a plant FAE1 (fatty acid
XX elongation 1) gene. Nucleic acid constructs comprising transcriptional
XX regulatory regions homologous to plant FAE1 promoters may be used to
XX transgenic cells or plants to promote expression of foretin and
XX endogenous genes in developing seeds. The constructs are used to affect
XX expression of foretin and endogenous genes in developing seeds and
XX seed lipid metabolism, protein or carbohydrate composition and
XX accumulation, or seed development. Transcriptional regulatory regions of
XX the FAE1 gene may be useful for the production of modified seeds
XX containing novel recombinant proteins which have pharmaceutical
XX industrial or nutritional value. The nucleic acids may also be used as
XX plant breeding tools, as molecular markers to aid in plant breeding
XX programmes. Such techniques include using the gene as a molecular probe
XX or using the FAE1 sequence to design PCR primers for use in screening
XX techniques.

XX Sequence 393 bp; 138 A; 65 C; 59 G; 141 T; 0 other;

XX Query Match 100.0%; Score 393; DB 22; Length 393; 0; 0;
XX Host Local Similarity 100.0%; Pred. No. 2, 46-76; Indels 0; Gaps 0;
XX Matches 393; Conservative 0; Mismatches 0

XX 1 aaactaaagacacacattccctgaattttaaagacatataatcaatattatgacaa 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1 aaactaaagacacacattccctgaattttaaagacatataatcaatattatgacaa 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 61 ttcaaaataatgaatataaagacacacacacacacacacacacacacacacac 120
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 61 ttcaaaataatgaatataaagacacacacacacacacacacacacacacacac 120
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 61 ttcaaaataatgaatataaagacacacacacacacacacacacacacacacac 180
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 121 aaactaaatgaatataatataatataatataatataatataatataatataat 240
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 121 aaactaaatgaatataatataatataatataatataatataatataatataat 240
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 181 taagaattatataatataatataatataatataatataatataatataatataat 240
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 181 taagaattatataatataatataatataatataatataatataatataatataat 240
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 241 aaactaaatgaatataatataatataatataatataatataatataatataat 300
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 241 aaactaaatgaatataatataatataatataatataatataatataatataat 300
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 301 ttcaaaataatgaatataatataatataatataatataatataatataatataat 360
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 301 ttcaaaataatgaatataatataatataatataatataatataatataatataat 360
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 361 ctctccatatttttccgacacacacacacacacacacacacacacacacacac 393
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 361 ctctccatatttttccgacacacacacacacacacacacacacacacacacac 393
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 2

AAFe2747

ID AAF62737 standard: DNA, 900 bp.

XX AAF62737:

XX 02-MAY-2001 (first entry)

XX Plant FAE1 gene 5' region #2.

XX FAE1: fatty acid elongation 1; seed-specific gene expression;

XX transgenic plant; seed development; seed lipid metabolism; ds.

XX Plantae.

XX W0200111061-A2.

PF 15-FEB-2001.

XX 04-AUG-2000; 2000WD-CA00907.

XX 04-AUG-1999; 9908-0147133.

XX (USBR) UNIV BRITISH COLUMBIA.

XX Kunst L; Clemens S;

XX WPI: 2001-191548/19.

XX Recombinant nucleic acid for mediating seed specific expression in

XX Arabidopsis, comprises a heterologous promoter with a transcriptional

XX regulatory region of the 5' region of a plant fatty acid elongation 1

XX gene.

XX claim 3: Page 18-19: 41pp: English.

XX The present sequence is the 5' region of a plant FAE1 (fatty acid
XX elongation 1) gene. Nucleic acid constructs comprising transcriptional
XX regulatory regions homologous to plant FAE1 promoters may be used to
XX transgenic cells or plants to promote expression of foretin and
XX endogenous genes in developing seeds. The constructs are used to affect
XX expression of foretin and endogenous genes in developing seeds and
XX seed lipid metabolism, protein or carbohydrate composition and
XX accumulation, or seed development. Transcriptional regulatory regions of
XX the FAE1 gene may be useful for the production of modified seeds
XX containing novel recombinant proteins which have pharmaceutical
XX industrial or nutritional value. The nucleic acids may also be used as
XX plant breeding tools, as molecular markers to aid in plant breeding
XX programmes. Such techniques include using the gene as a molecular probe
XX or using the FAE1 sequence to design PCR primers for use in screening
XX techniques.

XX Sequence 900 bp; 313 A; 142 C; 156 G; 289 T; 0 other;

XX Query Match 100.0%; Score 393; DB 22; Length 900;
XX Host Local Similarity 100.0%; Pred. No. 2, 46-76; Indels 0; Gaps 0;
XX Matches 393; Conservative 0; Mismatches 0

XX 1 aaactaaagacacacattccctgaattttaaagacatataatcaatattatgacaa 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 508 aaactaaagacacacattccctgaattttaaagacatataatcaatattatgacaa 60
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 61 ttcaaaataatgaatataaagacacacacacacacacacacacacacacacac 120
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 61 ttcaaaataatgaatataaagacacacacacacacacacacacacacacacac 120
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 61 ttcaaaataatgaatataaagacacacacacacacacacacacacacacacac 180
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 121 aaactaaatgaatataatataatataatataatataatataatataatataat 240
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 121 aaactaaatgaatataatataatataatataatataatataatataatataat 240
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 181 taagaattatataatataatataatataatataatataatataatataatataat 240
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 181 taagaattatataatataatataatataatataatataatataatataatataat 240
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 241 aaactaaatgaatataatataatataatataatataatataatataatataat 300
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 241 aaactaaatgaatataatataatataatataatataatataatataatataat 300
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 301 ttcaaaataatgaatataatataatataatataatataatataatataatataat 360
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 301 ttcaaaataatgaatataatataatataatataatataatataatataatataat 360
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 361 ctctccatatttttccgacacacacacacacacacacacacacacacacacac 393
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 361 ctctccatatttttccgacacacacacacacacacacacacacacacacacac 393
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 608 taagaattatataatataatataatataatataatataatataatataatataat 667
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 608 taagaattatataatataatataatataatataatataatataatataatataat 667
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 668 aaactaaatgaatataatataatataatataatataatataatataatataat 727
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 668 aaactaaatgaatataatataatataatataatataatataatataatataat 727
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 729 aaactaaatgaatataatataatataatataatataatataatataatataat 788
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 729 aaactaaatgaatataatataatataatataatataatataatataatataat 788
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 808 taagaattatataatataatataatataatataatataatataatataatataat 867
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 808 taagaattatataatataatataatataatataatataatataatataatataat 867
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 868 ctctccatatttttccgacacacacacacacacacacacacacacacacacac 900
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 3

AAFe2740

RESULT 1 9
 ID AAZ35524 standard; DNA: 1792 BP.
 XX
 AC AAZ35524;
 XX
 DT 01-FEB-2000 (first entry)
 XX
 DE Fatty acid elongase gene FAE-1.
 XX
 KW Fatty acid elongase; FAE-1; stomatal guard cells; promoter; stomatal
 XX transpiration factor; cotton; tobacco; citrus plant; nut plant; insect;
 KW resistance; tolerance; herbicide; desiccation; fungal infection;
 XX viral infection; bacterial infection; SS.
 XX
 OS Arabidopsis thaliana.
 XX
 PN W69954471-A1.
 XX
 PD 28-OCT-1999.
 XX
 PE 19-APR-1999; 99WD-GB01191.
 XX
 PR 20-APR-1998; 98GH-0008304.
 XX
 PT (GENE.) ZENECA LTD.
 XX
 PU Van der Lee FM, Sijmons PC, Hetherington AM, Holroyd GH, Gray JE:
 XX WPI: 2000-013454/01.
 XX
 PI Novel polynucleotide sequences used to produce plants with increased
 PT numbers of stomata -
 XX
 PS Claim 2: Page 46-37: 45pp, English.
 XX
 SM This sequence is the fatty acid elongase gene FAE-1 from Arabidopsis
 CC thaliana. The FAE-1 sequence can act as a stomatal guard cell specific
 CC promoter. The sequence is used in the invention which relates to a method
 CC for producing plants with increased numbers of stomata. The method
 CC involves inhibiting, in plant material, the production of fatty acids
 CC which stimulate the synthesis of the 14-18 classes of trans-lipid
 CC factors, or preventing the fatty acids from stimulating the synthesis of
 CC these factors (via disruption via 32P-1 gene); selecting the inhibited
 CC material; regenerating plants from it; and selecting plants with
 CC increased numbers of stomata. The sequence can also be used to produce a
 CC vector which can be introduced into plant cells to increase stomatal
 CC expression. The methods are used to produce plants with increased numbers
 CC of stomata on their leaves. Plants which can be used in the methods of
 CC the invention include soybean, cotton, tobacco, sunflower, oilseed rape,
 CC canola, flax, sunflower, potato, alfalfa, lettuce, maize, wheat,
 CC sorghum, rice, banana, barley, oat, turf grass, forage grass, sugar cane,
 CC pea, field bean, rice, pine poplar, apple, grape, citrus, or nut plant.
 CC poppers, citrus and nut plants. The plants may also be transformed with
 CC genes which provide resistance or tolerance to herbicides, insects,
 CC desiccation and/or fungal, bacterial or viral infections.
 XX
 SQ Sequence 1792 BP; 501 A; 377 G; 373 G; 541 T; 0 of 641;

DISCUSSION

The present investigation has shown that the

and/or single nucleotide polymorphisms.

PN	WO/2002/0928-A2.
PP	
PP	03-JAN-2002.
XX	
PP	02-JUL-2001; 2001WO-EP07537.
XX	
PP	30-JUN-2000; 2000DE-1032529.
PP	01-SEP-2000; 2000DE-1043626.
XX	
PP	(EPIC-) EPIGENOMICS AG.
XX	
PP	Olek A. Piepenbrock C., Berlin K;
XX	
PP	WP1: 2002-130909/17.
PP	
PP	Nucleic acid comprising a fragment of chemically modified group, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.
PP	
XX	
PP	claim 1; SEQ ID No.1-3, 32pp + Sequence Listing; Germany.
PP	
PP	The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, age-related macular and macular degeneration, arteriosclerosis, anaemia, cancer, autoimmune diseases, leukæmia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and immunoregulatory diseases, for example.
PP	
PP	The present sequence is a clone of the invention.
XX	
PP	Sequence 7990 BP; 2223 A; 102 C; 1567 G; 4098 T; 9 other;

[illegible]

Search completed: June 4, 2002, 20:26:08
Job time: 4935 sec